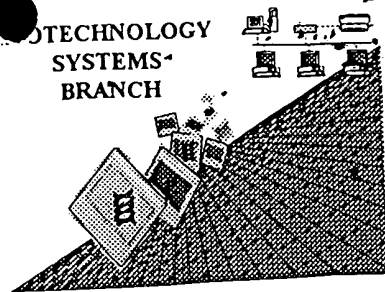


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



Q590
0919

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/767764
Source: OIPE
Date Processed by STIC: 09/21/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/267764

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PT

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned (Amino
Numbering ~~The numbering under each amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.~~ nucleotide
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length. Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/767,764

DATE: 09/21/2001
 TIME: 17:34:54

Input Set : A:\SeqList.txt
 Output Set: N:\CRF3\09212001\I767764.raw

3 <110> APPLICANT: Church, George
 5 <120> TITLE OF INVENTION: Method Of Making Protein Arrays
 7 <130> FILE REFERENCE: 10498-00009
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/767,764
 C--> 9 <141> CURRENT FILING DATE: 2001-01-23
 9 <150> PRIOR APPLICATION NUMBER: US 09/522,732
 11 <151> PRIOR FILING DATE: 2000-03-10
 13 <160> NUMBER OF SEQ ID NOS: 21
 15 <170> SOFTWARE: PatentIn version 3.0

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 24
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Bacteriophage T7
 22 <400> SEQUENCE: 1
 E--> 23 ~~taatacgaact cacta ca~~ (17)
 E--> 24 ~~24~~
 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 24
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 33 <221> NAME/KEY: misc_feature
 34 <222> LOCATION: ()..()
 35 <223> OTHER INFORMATION: Amplification primer.
 37 <400> SEQUENCE: 2
 E--> 38 ~~cactacgcc tccgtttcc tctc~~
 39 ~~24~~
 42 <210> SEQ ID NO: 3
 43 <211> LENGTH: 23
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <221> NAME/KEY: misc_feature
 50 <222> LOCATION: ()..()
 51 <223> OTHER INFORMATION: Amplification primer.
 53 <400> SEQUENCE: 3
 E--> 54 ~~ctgccccggg ttgctcattc tct~~
 55 ~~23~~
 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 24
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Artificial Sequence
 63 <220> FEATURE:

See Error Summary Sheet
 See pages 1 and 2

misaligned alignment - Invalid nucleotide numbering
 Global Errors

invalid alignment - Invalid nucleotide numbering
~~not to~~

Invalid nucleotide numbering MH

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/767,764

DATE: 09/21/2001

TIME: 17:34:54

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\09212001\I767764.raw

```
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <221> NAME/KEY: misc_feature
134 <222> LOCATION: ()..()
135 <223> OTHER INFORMATION: Amplification primer.
137 <400> SEQUENCE: 8
E--> 138 gggcggaagc ttgaaggagg tatttaagga gaaaataccg catcagg
139          47
142 <210> SEQ ID NO: 9
143 <211> LENGTH: 44
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <221> NAME/KEY: misc_feature
149 <222> LOCATION: ()..()
150 <223> OTHER INFORMATION: Amplification primer.
154 <400> SEQUENCE: 9
E--> 155 gcccggtctc gagcgtctgt ttacaccgat cgcccttccc aaca
156          44
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 47
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: ()..()
167 <223> OTHER INFORMATION: Amplification primer.
169 <400> SEQUENCE: 10
E--> 170 gcccggtctc gagcgtctgt ttaaattcac tggcgcgtgt ttacaa
171          47
174 <210> SEQ ID NO: 11
175 <211> LENGTH: 45
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
W--> 179 <220> FEATURE:
W--> 179 <223> OTHER INFORMATION:
179 <400> SEQUENCE: 11
E--> 180 gcccggtctc gagcgtctgt ttaccaatac gcaaaccgcc tctcc
181          45
184 <210> SEQ ID NO: 12
185 <211> LENGTH: 48
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: ()..()
192 <223> OTHER INFORMATION: Amplification primer.
195 <400> SEQUENCE: 12
E--> 196 ccactacgcc tccgctttcc tctcggggcg aagcttgaag gaggtatt
```

RAW SEQUENCE LISTING

DATE: 09/21/2001

PATENT APPLICATION: US/09/767,764

TIME: 17:34:54

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\09212001\I767764.raw

```

197          48
200 <210> SEQ ID NO: 13
201 <211> LENGTH: 46
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <221> NAME/KEY: misc_feature
207 <222> LOCATION: ()..()
208 <223> OTHER INFORMATION: Amplification primer.
210 <400> SEQUENCE: 13
E--> 211 ctgccccggg ttcctcattc tctgcccggg ctcgagcgtc tgttta
212          46
215 <210> SEQ ID NO: 14
216 <211> LENGTH: 10
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <221> NAME/KEY: misc_feature
222 <222> LOCATION: ()..()
223 <223> OTHER INFORMATION: Oligonucleotide for array templating.
225 <400> SEQUENCE: 14
E--> 226 tgcattgctat
227          10
230 <210> SEQ ID NO: 15
231 <211> LENGTH: 25
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <221> NAME/KEY: misc_feature
237 <222> LOCATION: ()..()
238 <223> OTHER INFORMATION: Oligonucleotide for array templating.
243 <400> SEQUENCE: 15
E--> 244 cgatgcattt acgtaacgta cgata
245          25
248 <210> SEQ ID NO: 16
249 <211> LENGTH: 32
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <221> NAME/KEY: misc_feature
255 <222> LOCATION: ()..()
256 <223> OTHER INFORMATION: Primer for in-situ amplification.
258 <220> FEATURE:
259 <221> NAME/KEY: misc_feature
260 <222> LOCATION: (27)..(32)<223> N can be a, c, g, or t.
262 <400> SEQUENCE: 16
E--> 263 gcagcagtag gactagcata tccgacnnnn nn
264          32
267 <210> SEQ ID NO: 17

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/767,764

DATE: 09/21/2001

TIME: 17:34:54

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\09212001\I767764.raw

```

268 <211> LENGTH: 32
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <221> NAME/KEY: misc_feature
274 <222> LOCATION: ()..()
275 <223> OTHER INFORMATION: Primer for in-situ amplification.
277 <220> FEATURE:
278 <221> NAME/KEY: misc_feature
279 <222> LOCATION: (27)..(32)
280 <223> OTHER INFORMATION: N can be a, c, g, or t.
282 <400> SEQUENCE: 17
E--> 283 cgatagcagt agcatgcagg tccgacnnnn nn
      32
286 <210> SEQ ID NO: 18
287 <211> LENGTH: 66
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <221> NAME/KEY: misc_feature
293 <222> LOCATION: ()..()
294 <223> OTHER INFORMATION: Prophetic example of genomic DNA sequence.
296 <400> SEQUENCE: 18
E--> 297 tccggtcacc tgcagtctgc cagcagtcgg actacgtacc ccggtacgtg cgctacacgc
      60
E--> 300 agctttt
      66
304 <210> SEQ ID NO: 19
305 <211> LENGTH: 88
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial sequence
W--> 308 <220> FEATURE:
309 <221> NAME/KEY: misc_feature
310 <222> LOCATION: ()..()
311 <223> OTHER INFORMATION: Primer for in-situ amplification.
313 <400> SEQUENCE: 19
E--> 314 gcagcagtag gactagcata tccgacctgc gtgtagcgca cgtaccgggg tacgtagtcc
      60
E--> 317 gactgctggc agcatgcaga tgagccga
      88
321 <210> SEQ ID NO: 20
322 <211> LENGTH: 94
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <221> NAME/KEY: misc_feature
328 <222> LOCATION: ()..()
329 <223> OTHER INFORMATION: Primer for in-situ hybridization.
332 <400> SEQUENCE: 20

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/767,764

DATE: 09/21/2001

TIME: 17:34:54

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\09212001\I767764.raw

```
E--> 333 cgatagcagt agcatgcagg tccgaccagc agtcggacta cgtaccccggt tacgtgcgct
      334                60
E--> 336 acacgcaggt cggatatgct agtcgtactg ctgc
      337                94
      339 <210> SEQ ID NO: 21
      340 <211> LENGTH: 94
      341 <212> TYPE: DNA
      342 <213> ORGANISM: Artificial Sequence
      344 <220> FEATURE:
      345 <221> NAME/KEY: misc_feature
      346 <222> LOCATION: ()..()
      347 <223> OTHER INFORMATION: Primer for in-situ hybridization.
      349 <400> SEQUENCE: 21
E--> 350 gcagcagtac gactagcata tccgacctgc gtgtagcgca cgtaccgggg tacgtagtcc
      351                60
E--> 353 gactgctggt cggacctgca tgctactgct atcg
      354                94
```


VERIFICATION SUMMARY

DATE: 09/21/2001

PATENT APPLICATION: US/09/767,764

TIME: 17:34:55

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\09212001\I767764.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:1
M:254 Repeated in SeqNo=1
L:24 M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:17 SEQ:1
L:38 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:2
L:54 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:3
L:69 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:73 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:4
L:88 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:5
L:103 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:6
L:123 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:7
L:138 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:8
L:155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:44 SEQ:9
L:170 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:10
L:179 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:179 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:180 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:11
L:196 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:12
L:211 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:13
L:226 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:10 SEQ:14
L:244 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:15
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:263 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:16
L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:283 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:17
L:297 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:18
M:254 Repeated in SeqNo=18
L:308 M:283 W: Missing Blank Line separator, <220> field identifier
L:314 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
M:254 Repeated in SeqNo=19
L:333 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:20
M:254 Repeated in SeqNo=20
L:350 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:21
M:254 Repeated in SeqNo=21